

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:11:43 ; Search time 116.57 Seconds

(without alignments)  
390.303 Million cell updates/sec

Title: US-09-719-748-2\_COPY\_13\_275

Perfect score: 1343  
Sequence: 1 YDIGELGSGQFAIVKRCRE.....LVKETRRKRLTIOEALRHPWI 263

Scoring table:  
BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:.\*  
1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phage:.\*  
10: sp\_plant:.\*  
11: sp\_rodent:.\*  
12: sp\_virus:.\*  
13: sp\_vertebrate:.\*  
14: sp\_unclassified:.\*  
15: sp\_virus:.\*  
16: sp\_bacteriophage:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	1332	99.2	370 4 075892	075892 homo sapien
2	1321	98.4	370 4 091K4	091K4 homo sapien
3	1297	96.6	370 11 0901M4	0901M4 mus musculu
4	1128	84.0	1430 11 093J37	093J37 mus musculu
5	1125	83.8	345 11 09CV44	09CV44 mus musculu
6	1124	83.7	367 4 09BTL8	09BTL8 homo sapien
7	1121	83.5	454 4 043293	043293 homo sapien
8	1106	82.4	448 11 054784	054784 mus musculu
9	1106	82.4	448 11 088764	088764 ratu mus
10	1073	79.9	303 11 088861	088861 mus musculu
11	745.5	55.5	1435 5 044997	044997 caenorhabd
12	660.5	49.2	2762 5 P91255	P91255 caenorhabd
13	646.5	48.1	641 6 09HE69	09HE69 macaca fasc
14	642.5	47.8	992 4 09C015	09C015 homo sapien
15	636.5	47.4	907 13 098850	098850 carassius a
16	636	47.4	371 11 091X58	091X58 ratu mus

ID	Score	Query length	DB ID	Description
17	634	47.2	372 11 0923E7	0923E7 mus musculu
18	631.5	47.0	611 11 091XS9	091XS9 cavia porce
19	627.5	46.7	1721 5 0961U1	0961U1 drosophila
20	627.5	46.7	7107 5 09V4F7	09V4F7 drosophila
21	617.5	46.0	6658 5 076281	076281 drosophila
22	607.5	45.2	451 5 016980	016980 aplysia cal
23	599.5	44.6	795 4 096BV1	096BV1 homo sapien
24	577.5	43.0	1211 5 023260	023260 caenorhabd
25	576.5	42.9	446 5 095SK9	095SK9 drosophila
26	575	42.8	929 5 001651	001651 drosophila
27	574	42.7	577 5 096V81	096V81 drosophila
28	574	42.7	732 5 096V71	096V71 drosophila
29	574	42.7	786 5 096V79	096V79 drosophila
30	574	42.7	832 5 001653	001653 drosophila
31	574	42.7	913 5 09V7G6	09V7G6 drosophila
32	574	42.7	1289 4 09V2A5	09V2A5 homo sapien
33	573	42.7	2959 11 09V1F1	09V1F1 ratu mus
34	569.5	42.4	596 4 09H1R3	09H1R3 homo sapien
35	566	42.1	569 5 001652	001652 drosophila
36	562.5	41.9	6831 5 023550	023550 caenorhabd
37	562.5	41.9	7160 5 023551	023551 caenorhabd
38	557.5	41.5	335 5 061269	061269 mytilus gal
39	557.5	41.5	878 5 09GV22	09GV22 mytilus gal
40	541	40.3	4650 4 015598	015598 homo sapien
41	541	40.3	26926 4 010466	010466 homo sapien
42	538	40.1	775 6 09V754	09V754 oryctolagus
43	537	40.0	623 5 09GV80	09GV80 drosophila
44	525	39.1	638 5 09VYX9	09VYX9 drosophila
45	521	38.8	980 10 09LOR4	09LOR4 arabidopsis

## ALIGNMENTS

ID	Score	Query length	DB ID	Description
AC	075892	PRELIMINARY:	PRT:	370 AA.
DT	075892	075892		
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	DAP-KINASE RELATED PROTEIN 1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=KIDNEY;			
RX	MEDLINE=20094983; PubMed=10629061;			
RA	Imbal B., Shant G., Cohen O., Kissil J.L., Kimchi A.;			
RT	Death-associated protein kinase-related protein 1, a novel			
RT	Serine/threonine kinase involved in apoptosis.*;			
RL	Mol. Cell. Biol. 20:1044-1054(2000).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL: AF052941; AAC35001.1;			
DR	HSP, Q63450; 1A06.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_pkinase.			
DR	Pfam: PF00069; pkinase; 1.			
DR	SMART: SM00220; S_TKc; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SO	SEQUENCE 370 AA; 42923 MW; 09502B4DCDD20F91 CRC64;			

Query Match 99.2%; Score 1332; DB 4; Length 370;  
Best Local Similarity 99.6%; Pred. No. 1.5e-95;  
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YDIGELGSGQFAIVKRCREKSTGLEYAKFKIKRGRASRRGVSNHEIEREVSILROYL 60